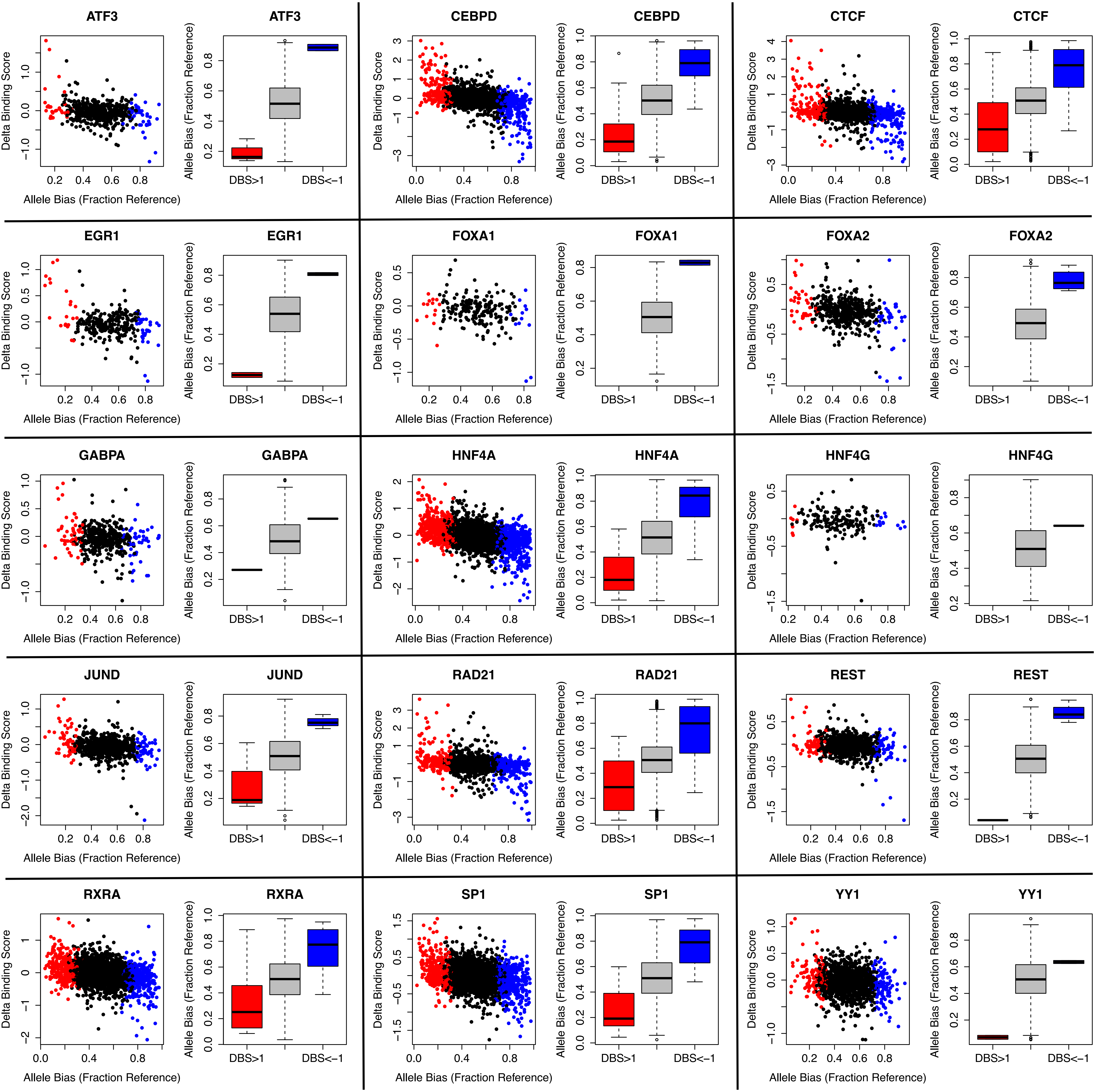

Supplemental_Fig_S18. Paneled pairs of plots for each DAP overlapping at least one SNP with significant allele bias and at least one SNP with a delta binding score falling in the top percentile (15/20). The left figure for each factor is a scatterplot demonstrating the correlation between delta binding score and the observed ChIP-seq allele bias at heterozygous SNPs overlapping a binding site. Red points indicate SNPs with significant bias towards an alternate allele, blue points indicate bias towards the reference allele, and black points indicate no significant allele bias was observed. The right figure consists of boxplots of binding site-overlapping heterozygous SNPs predicted to be in the top ~1% for decreasing binding affinity (red), to be in the top ~1% for increasing binding affinity (blue), and to have no significant impact on binding affinity (black). Y-axis indicates the fraction of ChIP reads mapping to the reference allele.